

amdt/B
#5



SEQUENCE LISTING

<110> BECQUART, JEROME

<120> ALBUMIN DERIVATIVES WITH THERAPEUTIC FUNCTIONS

<130> 06832.1429-03

<140> 10/073,118

<141> 2002-02-12

<150> 09/551,635

<151> 2000-04-18

<150> 09/004,319

<151> 1998-01-08

<150> 08/479,146

<151> 1995-06-07

<150> 08/295,078

<151> 1994-08-26

<150> 08/121,236

<151> 1993-09-13

<150> 07/955,243

<151> 1992-10-01

<150> 07/561,879

<151> 1990-08-02

<150> FR 89 10480

<151> 1989-08-03

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 13

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
restriction site

<220>

<221> modified_base

<222> (5)..(9)

<223> a, c, t, g, other unknown

<400> 1

ggccnnnnng gcc

B1

<210> 2
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

<400> 2
 atctaaggaa atacaagctt atgaagtggg t 31

<210> 3
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 3
 taaaaacaaa agatccccaa gcttggggat ctcccatgtc tctact 46

<210> 4
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 adaptor

<400> 4
 gatccgtcga cg 12

<210> 5
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 5
 aagctttaca acaaataataa aaacaatg 28

<210> 6
 <211> 73
 <212> DNA
 <213> Artificial Sequence

B1

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 6

ttacattatt aattttaaaaa tggatttcaa agataaggct ttaaattgatc taaggccgcg 60
attaaattcc aac 73

<210> 7

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 7

ccttaggctt ataacatcac atttaaaagc atctcagcct accatgagaa taagagaaag 60
aaaatgaaga tcaaaagctt 80

<210> 8

<211> 31

<212> DNA

<213> Artificial Sequence

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oligodeoxynucleotide

<400> 8

gtgtttcgtc gagacgccca caagagtgag g 31

<210> 9

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligodeoxynucleotide

<400> 9

ggtgtgtttc gtagatctgc acacaagagt gagg 34

<210> 10

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligodeoxynucleotide

<400> 10
 ccaggggtgt gtttcgtcga aagaaagtgg tgctgggc 38

<210> 11
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

<400> 11
 ccaactctga caccgacgcc cacctgcttc agg 33

<210> 12
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

<400> 12
 gctagctttc gacgccgggg gaattcg 27

<210> 13
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

<400> 13
 gcagaaccag aaggacgcca aggtggagtt c 31

<210> 14
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

<400> 14
 gaaatgcata agctcttgcc attctcacgg 30

<210> 15
 <211> 51

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

 <400> 15
 actgccaact ctgacaccta aaagcttgga tcccacctgc ttcaggggca g 51

 <210> 16
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

 <400> 16
 ggtaggtcgt gtggacgcc a gatctttgga aagaattgcc cgtctggaag 50

 <210> 17
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

 <400> 17
 ctgcaggta ggcgtcgcca accagttgct tcagctgtgc 40

 <210> 18
 <211> 12
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

 <400> 18
 gatcccctaa gg 12

 <210> 19
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

<400> 19
 gtgctgggca aacaagggga tacag 25

<210> 20
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

<400> 20
 ggcttaaagc aagtgggtgct g 21

<210> 21
 <211> 69
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

<400> 21
 tgctttgccg aggagggtaa ggaagacgct aagggtgaagt ctgaagaaga agccttaggc 60
 ttaaagaaa 69

<210> 22
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

<400> 22
 cccgggaagc ttccttaggc ttaaagaaag tgggtgctggg caaaaaaggg 50

<210> 23
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligodeoxynucleotide

<400> 23
 cccgggaagc ttttagaaag ctagcaccac gatgtctat 39

<210> 24
 <211> 563
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: MstII-SmaI
 restriction fragment including the V1 and V2
 domains of the CD4 receptor of the HIV-1 virus

<400> 24
 ccttaggctt aaagaaagtgtgtgctgggca aaaaagggga tacagtggaa ctgacctgta 60
 cagcttccca gaagaagagc atacaattcc actggaaaaa ctccaaccag ataaagattc 120
 tgggaaatca gggctccttc ttaactaaag gtccatccaa gctgaatgat cgcgctgact 180
 caagaagaag cctttgggac caaggaaact tccccctgat catcaagaat cttaagatag 240
 aagactcaga tacttacatc tgtgaagtgg aggaccagaa ggaggagggtg caattgctag 300
 tgttcggatt gactgccaac tctgacaccc acctgcttca ggggcagagc ctgaccctga 360
 ccttgagagag cccccctggt agtagccctt cagtgcattg taggagtcca aggggtaaaa 420
 acatacaggg ggggaagacc ctctccgtgt ctcagctgga gctccaggat agtggcacct 480
 ggacatgcac tgtcttgacag aaccagaaga aggtggagtt caaaatagac atcgtgggtgc 540
 tagctttcta aaagcttccc ggg 563

<210> 25
 <211> 2379
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Restriction
 fragment HindIII coding for the protein fusion
 prepro-HSA-V1V2

<220>
 <221> CDS
 <222> (7)..(2370)

<400> 25
 aagctt atg aag tgg gta acc ttt att tcc ctt ctt ttt ctc ttt agc 48
 Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser
 1 5 10
 tcg gct tat tcc agg ggt gtg ttt cgt cga gat gca cac aag agt gag 96
 Ser Ala Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu
 15 20 25 30
 gtt gct cat cgg ttt aaa gat ttg gga gaa gaa aat ttc aaa gcc ttg 144
 Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu
 35 40 45
 gtg ttg att gcc ttt gct cag tat ctt cag cag tgt cca ttt gaa gat 192
 Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp
 50 55 60
 cat gta aaa tta gtg aat gaa gta act gaa ttt gca aaa aca tgt gtt 240
 His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val
 65 70 75

gct gat gag tca gct gaa aat tgt gac aaa tca ctt cat acc ctt ttt	288
Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe	
80 85 90	
gga gac aaa tta tgc aca gtt gca act ctt cgt gaa acc tat ggt gaa	336
Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu	
95 100 105 110	
atg gct gac tgc tgt gca aaa caa gaa cct gag aga aat gaa tgc ttc	384
Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe	
115 120 125	
ttg caa cac aaa gat gac aac cca aac ctc ccc cga ttg gtg aga cca	432
Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro	
130 135 140	
gag gtt gat gtg atg tgc act gct ttt cat gac aat gaa gag aca ttt	480
Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe	
145 150 155	
ttg aaa aaa tac tta tat gaa att gcc aga aga cat cct tac ttt tat	528
Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr	
160 165 170	
gcc ccg gaa ctc ctt ttc ttt gct aaa agg tat aaa gct gct ttt aca	576
Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr	
175 180 185 190	
gaa tgt tgc caa gct gct gat aaa gct gcc tgc ctg ttg cca aag ctc	624
Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu	
195 200 205	
gat gaa ctt cgg gat gaa ggg aag gct tcg tct gcc aaa cag aga ctc	672
Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu	
210 215 220	
aag tgt gcc agt ctc caa aaa ttt gga gaa aga gct ttc aaa gca tgg	720
Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp	
225 230 235	
gca gta gct cgc ctg agc cag aga ttt ccc aaa gct gag ttt gca gaa	768
Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu	
240 245 250	
gtt tcc aag tta gtg aca gat ctt acc aaa gtc cac acg gaa tgc tgc	816
Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys	
255 260 265 270	
cat gga gat ctg ctt gaa tgt gct gat gac agg gcg gac ctt gcc aag	864
His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys	
275 280 285	
tat atc tgt gaa aat caa gat tcg atc tcc agt aaa ctg aag gaa tgc	912
Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys	
290 295 300	

tgt gaa aaa cct ctg ttg gaa aaa tcc cac tgc att gcc gaa gtg gaa	960
Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu	
305 310 315	
aat gat gag atg cct gct gac ttg cct tca tta gct gct gat ttt gtt	1008
Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val	
320 325 330	
gaa agt aag gat gtt tgc aaa aac tat gct gag gca aag gat gtc ttc	1056
Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe	
335 340 345 350	
ctg ggc atg ttt ttg tat gaa tat gca aga agg cat cct gat tac tct	1104
Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser	
355 360 365	
gtc gta ctg ctg ctg aga ctt gcc aag aca tat gaa acc act cta gag	1152
Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu	
370 375 380	
aag tgc tgt gcc gct gca gat cct cat gaa tgc tat gcc aaa gtg ttc	1200
Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe	
385 390 395	
gat gaa ttt aaa cct ctt gtg gaa gag cct cag aat tta atc aaa caa	1248
Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln	
400 405 410	
aat tgt gag ctt ttt gag cag ctt gga gag tac aaa ttc cag aat gcg	1296
Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala	
415 420 425 430	
cta tta gtt cgt tac acc aag aaa gta ccc caa gtg tca act cca act	1344
Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr	
435 440 445	
ctt gta gag gtc tca aga aac cta gga aaa gtg ggc agc aaa tgt tgt	1392
Leu Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys	
450 455 460	
aaa cat cct gaa gca aaa aga atg ccc tgt gca gaa gac tat cta tcc	1440
Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser	
465 470 475	
gtg gtc ctg aac cag tta tgt gtg ttg cat gag aaa acg cca gta agt	1488
Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser	
480 485 490	
gac aga gtc acc aaa tgc tgc aca gaa tcc ttg gtg aac agg cga cca	1536
Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro	
495 500 505 510	
tgc ttt tca gct ctg gaa gtc gat gaa aca tac gtt ccc aaa gag ttt	1584
Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe	
515 520 525	

aat gct gaa aca ttc acc ttc cat gca gat ata tgc aca ctt tct gag	1632
Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu	
530 535 540	
aag gag aga caa atc aag aaa caa act gca ctt gtt gag ctt gtg aaa	1680
Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys	
545 550 555	
cac aag ccc aag gca aca aaa gag caa ctg aaa gct gtt atg gat gat	1728
His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp	
560 565 570	
ttc gca gct ttt gta gag aag tgc tgc aag gct gac gat aag gag acc	1776
Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr	
575 580 585 590	
tgc ttt gcc gag gag ggt aaa aaa ctt gtt gct gca agt caa gct gcc	1824
Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala	
595 600 605	
tta ggc tta aag aaa gtg gtg ctg ggc aaa aaa ggg gat aca gtg gaa	1872
Leu Gly Leu Lys Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu	
610 615 620	
ctg acc tgt aca gct tcc cag aag aag agc ata caa ttc cac tgg aaa	1920
Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys	
625 630 635	
aac tcc aac cag ata aag att ctg gga aat cag ggc tcc ttc tta act	1968
Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr	
640 645 650	
aaa ggt cca tcc aag ctg aat gat cgc gct gac tca aga aga agc ctt	2016
Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu	
655 660 665 670	
tgg gac caa gga aac ttc ccc ctg atc atc aag aat ctt aag ata gaa	2064
Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu	
675 680 685	
gac tca gat act tac atc tgt gaa gtg gag gac cag aag gag gag gtg	2112
Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val	
690 695 700	
caa ttg cta gtg ttc gga ttg act gcc aac tct gac acc cac ctg ctt	2160
Gln Leu Leu Val Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu	
705 710 715	
cag ggg cag agc ctg acc ctg acc ttg gag agc ccc cct ggt agt agc	2208
Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser	
720 725 730	
ccc tca gtg caa tgt agg agt cca agg ggt aaa aac ata cag ggg ggg	2256
Pro Ser Val Gln Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly	
735 740 745 750	

aag acc ctc tcc gtg tct cag ctg gag ctc cag gat agt ggc acc tgg 2304
 Lys Thr Leu Ser Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp
 755 760 765

aca tgc act gtc ttg cag aac cag aag aag gtg gag ttc aaa ata gac 2352
 Thr Cys Thr Val Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp
 770 775 780

atc gtg gtg cta gct ttc taaaagctt 2379
 Ile Val Val Leu Ala Phe
 785

<210> 26
 <211> 788
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Protein fusion
 prepro-HSA-V1V2

<400> 26
 Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
 1 5 10 15
 Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala
 20 25 30
 His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu
 35 40 45
 Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
 50 55 60
 Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
 65 70 75 80
 Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
 85 90 95
 Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
 100 105 110
 Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
 115 120 125
 His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
 130 135 140
 Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
 145 150 155 160
 Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
 165 170 175
 Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
 180 185 190

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
 195 200 205
 Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys
 210 215 220
 Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
 225 230 235 240
 Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
 245 250 255
 Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
 260 265 270
 Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
 275 280 285
 Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
 290 295 300
 Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
 305 310 315 320
 Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
 325 330 335
 Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
 340 345 350
 Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
 355 360 365
 Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
 370 375 380
 Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
 385 390 395 400
 Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
 405 410 415
 Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
 420 425 430
 Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val
 435 440 445
 Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
 450 455 460
 Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val
 465 470 475 480
 Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
 485 490 495

B₁

Val	Thr	Lys	Cys	Cys	Thr	Glu	Ser	Leu	Val	Asn	Arg	Arg	Pro	Cys	Phe	500	505	510
Ser	Ala	Leu	Glu	Val	Asp	Glu	Thr	Tyr	Val	Pro	Lys	Glu	Phe	Asn	Ala	515	520	525
Glu	Thr	Phe	Thr	Phe	His	Ala	Asp	Ile	Cys	Thr	Leu	Ser	Glu	Lys	Glu	530	535	540
Arg	Gln	Ile	Lys	Lys	Gln	Thr	Ala	Leu	Val	Glu	Leu	Val	Lys	His	Lys	545	550	555
Pro	Lys	Ala	Thr	Lys	Glu	Gln	Leu	Lys	Ala	Val	Met	Asp	Asp	Phe	Ala	565	570	575
Ala	Phe	Val	Glu	Lys	Cys	Cys	Lys	Ala	Asp	Asp	Lys	Glu	Thr	Cys	Phe	580	585	590
Ala	Glu	Glu	Gly	Lys	Lys	Leu	Val	Ala	Ala	Ser	Gln	Ala	Ala	Leu	Gly	595	600	605
Leu	Lys	Lys	Val	Val	Leu	Gly	Lys	Lys	Gly	Asp	Thr	Val	Glu	Leu	Thr	610	615	620
Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser	Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	625	630	635
Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn	Gln	Gly	Ser	Phe	Leu	Thr	Lys	Gly	645	650	655
Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala	Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	660	665	670
Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile	Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	675	680	685
Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu	Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	690	695	700
Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn	Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	705	710	715
Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu	Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	725	730	735
Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly	Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	740	745	750
Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu	Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	755	760	765
Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys	Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	770	775	780
Val	Leu	Ala	Phe													785		

<210> 27
 <211> 132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Leucine zipper
 of c-jun in a hybrid nucleotide HSA-CD4

<220>
 <221> CDS
 <222> (1)..(132)

<400> 27
 aga tct ttg gaa aga att gcc cgt ctg gaa gaa aaa gtg aaa act ctg 48
 Arg Ser Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
 1 5 10 15
 aaa gcc cag aac tct gag ctc gca tcc acg gcc aac atg ctg cgt gaa 96
 Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
 20 25 30
 cag gtt gca cag ctg aag caa ctg gtt ggc gac gcc 132
 Gln Val Ala Gln Leu Lys Gln Leu Val Gly Asp Ala
 35 40

<210> 28
 <211> 44
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Leucine zipper
 of c-jun in a hybrid protein HSA-CD4

<400> 28
 Arg Ser Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
 1 5 10 15
 Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
 20 25 30
 Gln Val Ala Gln Leu Lys Gln Leu Val Gly Asp Ala
 35 40

<210> 29
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<220>
 <221> CDS
 <222> (1)..(36)

<400> 29
 tgc ttt tca gct ctg gaa gtc gat gaa aca tac gtt
 Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val
 1 5 10

36

<210> 30
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 30
 Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val
 1 5 10

<210> 31
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<220>
 <221> CDS
 <222> (1)..(27)

<400> 31
 tca gct ctg gaa gtc gat gcc tta ggn
 Ser Ala Leu Glu Val Asp Ala Leu Gly
 1 5

27

<210> 32
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 32
 Cys Phe Ser Ala Leu Glu Val Asp Ala Leu Gly
 1 5 10

<210> 33
 <211> 35
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 33
 Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala
 1 5 10 15
 Leu Gly Leu Lys Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu
 20 25 30
 Leu Thr Cys
 35

<210> 34
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <221> MOD_RES
 <222> (2)
 <223> Ser, Pro, Thr or Ala

<220>
 <221> MOD_RES
 <222> (7)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (13)
 <223> Any amino acid

<400> 34
 Cys Xaa Leu Gly Leu Lys Xaa Val Val Leu Gly Lys Xaa Gly Asp Thr
 1 5 10 15
 Val Glu Leu Thr Cys
 20

<210> 35
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 35

Cys Phe Ala Glu Glu Gly Lys Glu Asp Ala Lys Gly Lys Ser Glu Glu
 1 5 10 15

Glu Ala Leu Gly Leu Lys Lys Val Val Leu Gly Lys Lys Gly Asp Thr
 20 25 30

<210> 36

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 36

Arg Gly Val Phe Arg Arg Lys Lys Val Val Leu Gly Lys Lys Gly Asp
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Thr Val Glu Leu Thr Cys
 20

<210> 37

<211> 22

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

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<223> Any amino acid

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<222> (14)

<223> Any amino acid

<400> 37

Arg Gly Val Phe Arg Arg Lys Xaa Val Val Leu Gly Lys Xaa Gly Asp
 1 5 10 15

Thr Val Glu Leu Thr Cys
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<210> 38

<211> 30

<212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 38

Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly
 1 5 10 15

Leu Thr Ala Asn Ser Asp Thr Asp Ala His Lys Ser Glu Val
 20 25 30

<210> 39

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 39

Cys Thr Val Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile
 1 5 10 15

Val Val Leu Ala Phe Asp Ala His Lys Ser Glu Val
 20 25

<210> 40

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 40

Cys Thr Val Leu Gln Asn Gln Lys Asp Ala His Lys Ser Glu Val
 1 5 10 15

<210> 41

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 41

Cys Asp Ala His Lys Ser Glu Val
 1 5

*B1
 cereus*